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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:23:21 ; Search time 52 seconds
(without alignments)
168.442 Million cell updates/sec

Title: US-09-852-238A-5
Perfect score: 164
Sequence: 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesepc_29Jan04:*
1: genesepc1980s:*
2: genesepc1990s:*
3: genesepc2000s:*
4: genesepc2001s:*
5: genesepc2002s:*
6: genesepc2003as:*
7: genesepc2003bs:*
8: genesepc2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	31	2 AAW39910	Aaw39910 Peptide r
2	164	100.0	100	2 AAW88231	Aaw88231 HIV-1 co-
3	164	100.0	184	2 AAW27406	Aaw27406 Inactive
4	164	100.0	215	2 AAW27408	Aaw27408 Inactive
5	164	100.0	215	2 AAW88238	Aaw88238 HIV-1 co-
6	164	100.0	268	7 ADC10142	Adc10142 Human NOV
7	164	100.0	268	7 ADC10144	Adc10144 Human NOV
8	164	100.0	352	2 AAW27407	Aaw27407 Human CCR
9	164	100.0	352	2 AAW27123	Aaw27123 Human che
10	164	100.0	352	2 AAW23835	Aaw23835 Human CC
11	164	100.0	352	2 AAW88232	Aaw88232 HIV-1 co-
12	164	100.0	352	4 AAE07048	Aae07048 Human G-p
13	164	100.0	352	4 AAG80111	Aag80111 Human CCR
14	164	100.0	352	4 AAE04321	Aae04321 Human che
15	164	100.0	352	4 AAE07039	Aae07039 Human G-p
16	164	100.0	352	4 AAB46858	Aab46858 Human HDG
17	164	100.0	352	4 AAB56342	Aab56342 Non-endog
18	164	100.0	352	4 AAB83354	Aab83354 Human CCR
19	164	100.0	352	4 AAB82948	Aab82948 Human HIV
20	164	100.0	352	5 AAU97152	Aau97152 Human G-p
21	164	100.0	352	5 AAM52829	Aam52829 Human CCR
22	164	100.0	352	5 AAM52828	Aam52828 Human CC
23	164	100.0	352	5 ABG70597	Abg70597 Human G-p
24	164	100.0	352	5 ABG92883	Abg92883 Human imm
25	164	100.0	352	5 AAE25811	Aae25811 Human G-p

ALIGNMENTS

RESULT 1

AAW39910
ID AAW39910 standard; peptide; 31 AA.
XX AC AAW39910;
XX
XX
DT 06-JUL-1998 (first entry)
XX
XX
DE Peptide representing an extracellular domain of C-C CKR-5.
XX
KW Chemokine receptor; C-C CKR-5; Human Immunodeficiency Virus; HIV-1;
KW CD4+ cell; inhibition; HIV-1 infection; beta-chemokine;
KW non-synctium-inducing HIV-1 strain; treatment.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9747319-A1.
PD 18-DEC-1997.
XX

PF 13-JUN-1997; 97WO-US010619.
XX

PR 14-JUN-1996; 96US-0019941P.
XX

PR 14-JUN-1996; 96US-00665090.
XX

PA (PROG-) PROGENICS PHARM INC.
XX

PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX

PI Allaway GP, Dragic T, Litwin VM, Maddon RJ, Moore JP, Trkola A;
XX

PI WPI; 1998-086551/08.
XX

PT Chemokine receptor CCR5 fragments - useful for inhibition of Human
XX

PT Immunodeficiency Virus 1 infection.
XX

XX
XX Disclosure; Page 2; 106pp; English.

XX
XX Synthetic peptides AAW39910-13 represent the 4 extracellular domains of
XX

XX human chemokine receptor C-C CKR-5, C-C CKR-5 is capable of inhibiting
XX

XX the fusion of Human Immunodeficiency Virus (HIV)-1 to CD4+ cells and thus
XX

XX inhibiting HIV-1 infection of the cells. It is suggested that C-C CKR-5
XX

XX functions as a beta-chemokine-sensitive second receptor for primary, non-
XX

XX synctium-inducing HIV-1 strains. The synthetic peptides were tested for
XX

XX their ability to inhibit membrane fusion mediated by the envelope
XX

XX glycoproteins of the LAI or JR-FL strains of HIV-1 using a resonance
XX

XX energy transfer assay. Specific inhibition of fusion mediated by the JR-
XX

XX FL envelope glycoprotein was seen using the ECL2 peptide but not other
XX

XX

XX

XX

CC peptides. Polypeptides capable of inhibiting the fusion of HIV-1 to CD4+
 CC cells are useful in the treatment of an HIV-1 infected subject.
 CC Antibodies against such proteins are also useful for inhibition of HIV-1
 CC infection of CD4+ cells

XX SQ Sequence 31 AA;
 Query Match 100.0%; Score 164; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 2
 AAW88231
 ID AAW88231 standard; protein; 100 AA.
 XX AC AAW88231;
 XX 15-MAR-1999 (first entry)
 DT HIV-1 co-receptor CCR5 variant CCR5m303.
 DE HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 XX HIV gene therapy; human.
 KW Homo sapiens.
 XX OS
 XX FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 XX WO9854317-A1.
 XX 03-DEC-1998.
 XX 29-MAY-1998; 98WO-EF003437.
 XX 30-MAY-1997; 97US-0048057P.
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI WPI: 1999-059835/05.
 DR N-PSDB; AAW88231.
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 XX Claim 2; Page 37; 55pp; English.

XX This is the amino acid sequence of a CCR5 variant protein, designated
 CC CCR5m303, that comprises the first two transmembrane domains of wild-type
 CC CCR5 (see AAW88232), but lacks transmembrane domains 3-7. CCR5 serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The presence of the CCR5m303 variant allele (see AAW84125) with
 CC the wild type CCR5 allele in an individual shows a positive correlation
 CC with resistance to infection with M-tropic HIV-1 strains, and may
 CC indicate slower progression of the disease. The detection of CCR5
 CC variants may be used to identify individuals at lower risk of infection
 CC relative to the general population who, if infected, may exhibit slower
 CC progression to AIDS. Probes and primers (see AAW84127-36) are provided
 CC for use in diagnostic methods for detecting the presence of such
 CC variants. A method is provided for inhibiting HIV-1 infection of a cell
 CC expressing the CCR5 receptor. This involves introducing a nucleic acid
 CC encoding a CCR5 variant into the cell, thereby reducing the number of
 CC functional CCR5 molecules present on the cell surface

XX SQ Sequence 100 AA;
 Query Match 100.0%; Score 164; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.7e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 3
 AAW27406
 ID AAW27406 standard; protein; 184 AA.
 XX AC AAW27406;
 XX 14-APR-1998 (first entry)
 DT Inactive human CCR5.
 DE Inactive; human Cys-Cys chemokine receptor-5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX OS Homo sapiens.
 XX WO9732019-A2.
 XX 04-SEP-1997.
 XX 28-FEB-1997; 97WO-BE000023.
 XX 01-MAR-1996; 96EP-00870021.
 PR 06-AUG-1996; 96EP-00870102.
 XX (EURO-) EUROSREEN SA.
 XX Samson M, Parmentier M, Vassart G, Libert F;
 DR WPI: 1997-479829/44.
 DR N-PSDB; AAT90116.
 XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX Claim 1; Fig 1a; 94pp; English.

XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1
 CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
 CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders. Subjects that express the
 CC inactive receptor have a predisposition, or resistance to HIV-1 and/or
 CC HIV-2

XX SQ Sequence 184 AA;
 Query Match 100.0%; Score 164; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 4
AAW27408
ID AAW27408 standard; protein; 215 AA.
XX
XX
AC AAW27408;
XX
XX
DT 14-APR-1998 (first entry)
XX
XX
DE Inactive human CCR5.
XX
XX
KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9732019-A2.
XX
XX
PD 04-SEP-1997.
XX
XX
PF 28-FEB-1997; 97WO-BE000023.
XX
XX
PR 01-MAR-1996; 96EP-00870021.
PR 06-AUG-1996; 96EP-00870102.
XX
XX
PA (EURO-) EUROSREEN SA.
XX
XX
PI Samson M, Parmentier M, Vassart G, Libert F;
XX
XX
DR WPI; 1997-479829/44.
DR N-PSDB; AAT90118.
XX
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT - disease and viral infection.
XX
XX
PS Claim 7; Fig 1d-e; 94pp; English.
XX
XX
CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
CC 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
CC viral infections, especially human immunodeficiency virus type 1 or type
CC 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
CC disorders. Subjects that express the inactive receptor have a
CC predisposition, or resistance to HIV-1 and/or HIV-2
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 164; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSPCKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYYTSPCKINVKQIAAR 31
RESULT 5
AAW8238
ID AAW8238 standard; protein; 215 AA.
XX
XX
AC AAW8238;
XX
XX
DT 15-MAR-1999 (first entry)
XX
XX
DE HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX

KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.
XX
XX
OS Homo sapiens.
XX
XX
PH Location/Qualifiers
FT Domain 32..56 /note= "transmembrane domain 1"
FT Domain 67..87 /note= "transmembrane domain 2"
FT Domain 103..124 /note= "transmembrane domain 3"
FT Domain 142..167 /note= "transmembrane domain 4"
XX
XX
PN WO9854317-A1.
XX
XX
PD 03-DEC-1998.
XX
XX
PF 29-MAY-1998; 98WO-EP003437.
XX
XX
PR 30-MAY-1997; 97US-0048057P.
XX
XX
PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
XX
PI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX
XX
DR WPI; 1999-059835/05.
DR N-PSDB; AAV84159.
XX
XX
PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
PT resistance of CCR5-expressing cells to HIV-1 infection.
XX
XX
PS Disclosure; Page 38-39; 55pp; English.
XX
XX
CC This is the amino acid sequence of a CCR5 variant protein, designated
CC CCR5-delta32, that includes the first 4 transmembrane domains of wild-
CC type CCR5 (see AAW8232), but lacks transmembrane domains 5-7. CCR5
CC serves as a co-receptor for infection by macrophage-tropic (M-tropic)
CC strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
CC are resistant to HIV-1 infection, but heterozygous individuals are
CC susceptible. The invention additionally relates to the identification of
CC variant CCR5m303 (see AAW8231), which lacks transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify individuals
CC at lower risk of infection relative to the general population who, if
CC infected, may exhibit slower progression to AIDS. Probes and primers (see
CC AAV84127-36) are provided for use in diagnostic methods for detecting the
CC presence of such variants. A method is provided for inhibiting HIV-1
CC infection of a cell expressing the CCR5 receptor. This involves
CC introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
CC reducing the number of functional CCR5 molecules present on the cell
CC surface
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 164; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSPCKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYYTSPCKINVKQIAAR 31
RESULT 6
ADC10142
ID ADC10142 standard; protein; 268 AA.
XX
XX
AC ADC10142;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Human NOVX polypeptide SEQ ID NO: 162.

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.
 XX Homo sapiens.

OS WO2003000842-A2.

XX 03-JAN-2003.

XX 04-JUN-2002; 2002WO-US017443.

XX 04-JUN-2001; 2001US-0295607P.

XX 06-JUN-2001; 2001US-0295661P.

XX 06-JUN-2001; 2001US-0296404P.

XX 06-JUN-2001; 2001US-0296418P.

XX 07-JUN-2001; 2001US-0296575P.

XX 11-JUN-2001; 2001US-0297414P.

XX 12-JUN-2001; 2001US-0295573P.

XX 12-JUN-2001; 2001US-0297567P.

XX 14-JUN-2001; 2001US-0298285P.

XX 15-JUN-2001; 2001US-0298528P.

XX 18-JUN-2001; 2001US-0299133P.

XX 19-JUN-2001; 2001US-0299230P.

XX 21-JUN-2001; 2001US-0299949P.

XX 22-JUN-2001; 2001US-0300177P.

XX 26-JUN-2001; 2001US-0300883P.

XX 28-JUN-2001; 2001US-0301530P.

XX 28-JUN-2001; 2001US-0301550P.

XX 03-JUL-2001; 2001US-0302951P.

XX 31-JUL-2001; 2001US-0308890P.

XX 14-SEP-2001; 2001US-0322297P.

XX 03-DEC-2001; 2001US-0324669P.

XX 14-SEP-2001; 2001US-0337477P.

XX 14-DEC-2001; 2001US-0341562P.

XX 21-FEB-2002; 2002US-0358656P.

XX 21-FEB-2002; 2002US-0359122P.

XX 22-FEB-2002; 2002US-0358978P.

XX 22-FEB-2002; 2002US-0359034P.

XX 03-JUL-2001; 2001US-0302951P.

XX 14-SEP-2001; 2001US-0322297P.

XX 03-DEC-2001; 2001US-0324669P.

XX 14-SEP-2001; 2001US-0337477P.

XX 14-DEC-2001; 2001US-0341562P.

XX 21-FEB-2002; 2002US-0358656P.

XX 21-FEB-2002; 2002US-0359122P.

XX 22-FEB-2002; 2002US-0358978P.

CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.
 XX

SQ Sequence 268 AA;

Query Match 100.0%; Score 164; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.2e-16;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYTSEPCOKINVKQIAAR 31

Db 1 MDYQVSSPIYDINYTSEPCOKINVKQIAAR 31

RESULT 7

ADCI0144

ID ADCI0144 standard; protein; 268 AA.

XX AC ADCI0144;

XX DT 18-DEC-2003 (first entry)

XX DE Human NOVX polypeptide SEQ ID NO: 164.

KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

OS Homo sapiens.

PN WO2003000842-A2.

PD 03-JAN-2003.

PF 04-JUN-2002; 2002WO-US017443.

XX 04-JUN-2001; 2001US-0295607P.

XX 04-JUN-2001; 2001US-0295661P.

XX 06-JUN-2001; 2001US-0296404P.

XX 06-JUN-2001; 2001US-0296418P.

XX 07-JUN-2001; 2001US-0296575P.

XX 11-JUN-2001; 2001US-0297414P.

XX 12-JUN-2001; 2001US-0295573P.

XX 12-JUN-2001; 2001US-0297567P.

XX 14-JUN-2001; 2001US-0298285P.

XX 15-JUN-2001; 2001US-0298528P.

XX 18-JUN-2001; 2001US-0299133P.

XX 19-JUN-2001; 2001US-0299230P.

XX 21-JUN-2001; 2001US-0299949P.

XX 22-JUN-2001; 2001US-0300177P.

XX 26-JUN-2001; 2001US-0300883P.

XX 28-JUN-2001; 2001US-0301530P.

XX 28-JUN-2001; 2001US-0301550P.

XX 31-JUL-2001; 2001US-0302951P.

PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dipippo VA, Edinger SR, Elserman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hsiao T, Ji W, Kekuda R;
 PI Khramtsov NV, Li L, Liu X, Malyankar DM, Miller CE, Millet I;
 PI Ort T, Padigaru M, Pattarajan M, Pena CE, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CE, Lepley DM;

XX WPI; 2003-210149/20.

XX N-PSDB; ADCI0141.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for

XX treating, preventing and diagnosing pathological conditions with NOVX-

XX associated disorders, such as cancer, obesity, diabetes and inflammatory

XX or CNS diseases.

XX Claim 1; SEQ ID NO 162; 772pp; English.


```

FT  /label= Extracellular_domain
FT  301..352
FT  /label= Intracellular_domain
XX
XX  WO9722698-A2.
XX  -26-JUN-1997.
XX
XX  20-DEC-1996; 96WO-US020759.
XX
XX  20-DEC-1995; 95US-00575967.
XX  07-JUN-1996; 96US-00661393.
XX
XX  (ICOS-) ICOS CORP.
XX
XX  Gray PW, Schweickart VL, Raport CJ;
XX  WPI; 1997-341689/31.
XX  N-PSDB; AAT85161.
XX
XX  New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX  modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX  tumours, viral infections, auto-immune diseases, etc.
XX
XX  Claim 16; Page 47-48; 65pp; English.
XX
XX  This polypeptide sequence comprises novel human chemokine receptor 88C, a
XX  G protein coupled receptor that is involved in leukocyte trafficking. Its
XX  amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
XX  macrophage library. It shows 62% identity to CCR5. Chemokine receptor
XX  88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
XX  and their polypeptide fragments can be produced in transformed host
XX  cells. The receptors, peptides comprising one or more of the
XX  extracellular or intracellular domains, and anti-receptor antibodies can
XX  be used to modulate receptor activities, particularly ligand and G
XX  protein binding, and are potentially potentially useful in the treatment
XX  of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX  infection, AIDS, inflammatory conditions, pathological immune response,
XX  abnormal haematopoietic processes etc
XX
XX  Sequence 352 AA;
XX  Query Match 100.0%; Score 164; DB 2; Length 352;
XX  Best Local Similarity 100.0%; Pred. No. 1.7e-16;
XX  Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MDYQVSSPIVDINITYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIVDINITYTSEPCQKINVKQIAAR 31
XX
RESULT 10
AAW23835
ID AAW23835 standard; protein; 352 AA.
XX
XX  AAW23835;
XX
XX  08-JUN-1998 (first entry)
XX
XX  Human CC chemokine receptor 5 (CCR5).
XX
XX  CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX  human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  29..55
XX  Domain /label= I
XX  /note= "transmembrane domain"
XX  104..126
XX  Domain /label= III
XX  /note= "transmembrane domain"
XX

```

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FT  Region
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FT  109..120
FT  Domain /label= IV
FT  143..171
FT  /note= "transmembrane domain"
FT  187..210
FT  /note= "extracellular loop-2 (Claim 19)"
FT  194..219
FT  Domain /label= V
FT  /note= "transmembrane domain"
FT  238..258
FT  Domain /label= VI
FT  /note= "transmembrane domain"
FT  261..276
FT  Region /note= "extracellular loop-3 (Claim 19)"
FT  277..300
FT  Domain /label= VII
FT  /note= "transmembrane domain"
FT
XX  WO9745543-A2.
XX
XX  04-DEC-1997.
XX
XX  28-MAY-1997; 97WO-US009586.
XX
XX  28-MAY-1996; 96US-0018508P.
XX
XX  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX  Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX  Broder CC, Kennedy PE;
XX  WPI; 1998-032650/03.
XX  N-PSDB; AAT76920.
XX
XX  CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX  between HIV and a target cell.
XX
XX  Claim 68; Fig 1C; 70pp; English.
XX
XX  This protein sequence comprises of a novel human macrophage-selective CC
XX  chemokine receptor that has been designated CCR5. The sequence was
XX  deduced from an isolated cDNA clone (see AAT76920). An Ala127Ileu variant
XX  (see W238340 of CCR5 was also identified. The susceptibility of human
XX  macrophages to HIV infection depends on cell surface expression of CD4
XX  and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX  protein coupled cell surface molecules. It plays an essential role in the
XX  membrane fusion step of infection by some HIV isolates. The establishment
XX  of stable, non-human cell lines and transgenic mammals having cells that
XX  coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX  infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX  agents capable of blocking membrane fusion between HIV and target cells
XX  represent potential anti-HIV therapeutics for macrophage tropic strains
XX  of HIV
XX
XX  Sequence 352 AA;
XX  Query Match 100.0%; Score 164; DB 2; Length 352;
XX  Best Local Similarity 100.0%; Pred. No. 1.7e-16;
XX  Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MDYQVSSPIVDINITYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIVDINITYTSEPCQKINVKQIAAR 31
XX
RESULT 11
AAW88232
ID AAW88232 standard; protein; 352 AA.
XX
XX  AAW88232;
XX
XX  15-MAR-1999 (first entry)
XX

```

XX HIV-1 co-receptor CCR5.
 XX
 XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CC5m303"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"
 FT Domain 200..223
 FT /note= "transmembrane domain 5"
 FT Domain 236..260
 FT /note= "transmembrane domain 6"
 FT Domain 275..301
 FT /note= "transmembrane domain 7"

XX WO9854317-A1.
 XX
 XX 03-DEC-1998.
 XX
 XX 29-MAY-1998; 98WO-EF003437.
 XX
 XX 30-MAY-1997; 97US-0048057P.
 XX
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI WPI; 1999-059835/05.
 DR N-PSDB; AAV84126.
 XX
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PT
 XX Disclosure; Page 34-35; 55pp; English.

XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW84231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 164; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINNYTSPQCINVKQIAAR 31
 ||||||||||||||||||||||||||||||||
 Db 1 MDYQVSSPIYDINNYTSPQCINVKQIAAR 31

RESULT 12
 AAE07048
 ID AAE07048 standard; protein; 352 AA.
 XX
 AC AAE07048;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytosatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200158916-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004153.
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488966/53.
 DR N-PSDB; AAD13299.
 XX
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 XX Example 40; Page 504-505; 518pp; English.
 XX
 XX The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX Sequence 352 AA;

Fri Jul 30 11:22:26 2004

us-09-852-238a-5.rag

Query Match 100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 13
AAG80111
ID AAG80111 standard; protein; 352 AA.
AC AAG80111;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR5 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PI 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IPF PHARM GMBH.
XX (FORS/) FORSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
XX WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 10; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR) which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 14
AAB04321
ID AAB04321 standard; protein; 352 AA.
XX
AC AAB04321;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
XX
KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
KW CC-CKR-5; envelope glycoprotein; anti-HIV.
XX
OS Homo sapiens.
XX
PN US6258527-B1.
XX
PD 10-JUL-2001.
XX
PF 21-MAY-1997; 97US-00861105.
XX
PR 20-MAY-1996; 96US-0017157P.
PR 19-JUN-1996; 96US-0020043P.
PR 19-MAY-1997; 97US-00858660.
XX
PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX (UUNY) UNIV NEW YORK STATE.
XX
PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
XX WPI; 2001-417127/44.
XX N-PSDB; AAD08577.
XX
PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
PT and HIV LTR for identification of drugs and antibodies for treatment of
PT HIV.
XX
PS Disclosure; Col 47-50; 37pp; English.
XX
CC The present invention relates to a transformed mammalian cell that
CC contains a gene encoding CD4, a construct encoding a reporter gene under
CC the regulation of an human immuno deficiency virus (HIV) long terminal
CC repeat (LTR) and that has been transduced with a vector encoding a human
CC chemokine receptor (CKR) where the CD4 and the CKR are present on the
CC cell surface of transformed mammalian cell. The invention is useful for
CC identifying drugs or antibodies that interfere with the translocation of
CC HIV into transformed mammalian cell or for identifying a human chemokine
CC receptor that facilitates the infection of a particular HIV strain into
CC the transformed mammalian cell. Compounds identified can be used to treat
CC cellular dysfunction and to prevent or combat HIV infection. The present
CC sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein.
CC CC-CKR-5 is the principal cofactor for entry mediated by the envelope
CC glycoproteins of primary macrophage-tropic strains of HIV-1
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 15
AAE07039

ID AAE07039 standard; protein; 352 AA.
 AC AAE07039;
 XX 16-OCT-2001 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 DE
 XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; neotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX

OS Homo sapiens.
 XX WO200158915-A2.
 PN 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX

PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX

PS Example 40; Page 486-487; 495pp; English.
 XX
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 CC protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation,
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX

SQ Sequence 352 AA;
 Query Match 100.0%; Score 164; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

Search completed: July 29, 2004, 13:28:33
 Job time : 53 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:26:01 ; Search time 16 Seconds
(without alignments)
186.371 Million cell updates/sec

Title: US-09-852-238A-5
Perfect score: 164
Sequence: 1 MDQVSSPIVDINYITSEPCQKINVKQLAAR 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	100.0	352	A43113	chemokine (C-C) re
2	57	34.8	178	T20317	hypothetical prote
3	54.5	33.2	130	T47540	actin depolymerizi
4	54	32.9	54	PT0189	protein-tyrosine k
5	54	32.9	211	B86864	uracil phosphoribo
6	54	32.9	617	AF1284	5-methyltetrahydro
7	54	32.9	617	AI1655	actin depolymerizi
8	53.5	32.6	132	G84717	conserved hypotet
9	52	32.3	516	T40181	E2 glycoprotein pr
10	52	31.7	1162	VGIHAK	hypothetical prote
11	51.5	31.4	818	T40491	probable exported
12	51	31.1	364	AE0169	E2 glycoprotein -
13	51	31.1	520	S14599	E2 glycoprotein pr
14	51	31.1	520	S14600	E2 glycoprotein -
15	51	31.1	520	S14598	spike protein chal
16	51	31.1	544	S41626	E2 glycoprotein pr
17	51	31.1	550	VGHD6	alpha-mannosidase
18	51	31.1	1130	T29089	E2 glycoprotein pr
19	51	31.1	1154	VGIHIB	E2 glycoprotein pr
20	51	31.1	1162	S14939	E2 glycoprotein pr
21	51	31.1	1162	S14940	laminin beta-1 cha
22	51	31.1	1790	MMFPB1	hypothetical prote
23	49.5	30.2	1039	T22982	protein F59B10.1
24	49.5	30.2	1192	H88293	chemokine (C-C) re
25	49	29.9	360	JC2443	chemokine (C-C) re
26	49	29.9	374	S38450	actin-depolymerizi
27	48.5	29.6	126	S30934	actin-depolymerizi
28	48.5	29.6	130	T05788	hypothetical prote
29	48.5	29.6	141	I36810	

ALIGNMENTS

RESULT 1

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A>Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:G1262810; PIDN:CAA62796.1; PID:G1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the A-CCR5 chemokine receptor gene
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSHLGAGPAACHGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99193; NID:G1524062; PIDN:CAA67767.1; PID:G1524063
A>Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection by conferring resistance to Yersinia plague infecti
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
R:Leukoc Biol 60, 147-152, 1996
J. Combadiere, C.; Ahuja, S.K.; Tiffany, H.D.; Murphy, P.M.
A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece
A:Reference number: A58833; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
Submitted to the EMBL Data Library May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A>Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

```

A/Accession: A58833
A/Molecule type: mRNA
A/Residues: 1-352 <RAP>
A/Cross-references: GB:U54994; NID:G1457945; PIDN:RAC50598.1; PID:G1457946
C/Comment: This is a receptor for chemokines MIP-1alpha (see FIR:A30574), MIP-1beta (see FIR:A30574), and dual-tropic strains of HIV-1 bind to a complex of chemokine (see FIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see FIR:A30574).
C/Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (see FIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see FIR:A30574).
C/Genetics:
A/Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A/Cross-references: GDB:I230510; OMIM:601373
A/Map position: 3p21-3p21
C/Description:
A/Note: probably acts to control granulocyte proliferation and differentiation
C/Superfamily: vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
F/32-56/Domain: transmembrane #status predicted <TM1>
F/67-87/Domain: transmembrane #status predicted <TM2>
F/103-124/Domain: transmembrane #status predicted <TM3>
F/142-166/Domain: transmembrane #status predicted <TM4>
F/193-218/Domain: transmembrane #status predicted <TM5>
F/236-257/Domain: transmembrane #status predicted <TM6>
F/285-300/Domain: transmembrane #status predicted <TM7>
F/20-269,101-178/Disulfide bonds: #status predicted
F/268/Binding site: carboxydrate (Asn) (covalent) #status predicted
F/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 164; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.4e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIVDINYYTSEPCQKINVKQIAAR 31
      |||||
DB 1 MDYQVSSPIVDINYYTSEPCQKINVKQIAAR 31
      |||||

RESULT 2
T20317
hypothetical protein D1081.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T20317
R/Dobson, R.
submitted to the EMBL Data Library, July 1996
A/Reference number: Z19256
A/Accession: T20317
A/Status: preliminary; translated from GB/EMBL/DBDJB
A/Molecule type: DNA
A/Residues: 1-178 <WIL>
A/Cross-references: EMBL:Z75710; PIDN:CAB00027.1; GSPDB:GN00019; CESP:D1081.6
A/Experimental source: clone D1081
C/Genetics:
A/Gene: CESP:D1081.6
A/Map position: 1
A/Introns: 95/3, 114/3

Query Match 34.8%; Score 57; DB 2; Length 178;
Best Local Similarity 52.9%; Pred. No. 0.94;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 QYVSSPIVDINYYTSEP 19
      :|||:|:|:|
DB 47 FQVQIPLYDLNIYAPEP 63

RESULT 3
T47540
actin depolymerizing factor 2 - Arabidopsis thaliana
N/Alternate names: protein F16L2.210
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C/Accession: T47540
C/Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;

```


Db 239 VDSKVSIVVDNSYTDK 256

RESULT 13

S14599

E2 glycoprotein - avian infectious bronchitis virus (strain UK/142/86) (fragment)

N;Alternate names: spike glycoprotein chain S1

C;Species: avian infectious bronchitis virus, IBV

A;Variety: strain UK/142/86

C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 20-Sep-1999

C;Accession: S14599

R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G. submitted to the EMBL Data Library, March 1991

A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some

A;Reference number: S14598

A;Accession: S14599

A;Status: preliminary

A;Molecule type: genomic RNA

A;Residues: 1-520 <CAV>

A;Cross-references: EMBL:X58066; NID:g59027; PIDN:CAA41097.1; PID:g59028

C;Superfamily: coronavirus E2 glycoprotein

Query Match 31.1%; Score 51; DB 2; Length 520;

Best Local Similarity 46.7%; Pred. No. 22;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 YDINYTSEPCQKIN 24

|-:|:|:|:|:|:|

Db 464 YGLNYYKVNPCEDVN 478

RESULT 14

S14600

E2 glycoprotein precursor - avian infectious bronchitis virus (strain UK/123/82) (fragment)

N;Alternate names: spike glycoprotein chain S1

C;Species: avian infectious bronchitis virus, IBV

A;Variety: strain UK/123/82

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 20-Sep-1999

C;Accession: S14600

R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G. submitted to the EMBL Data Library, March 1991

A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some

A;Reference number: S14598

A;Accession: S14600

A;Molecule type: Genomic RNA

A;Residues: 1-520 <CAV>

A;Cross-references: EMBL:X58067; NID:g59029; PIDN:CAA41098.1; PID:g59030

C;Superfamily: coronavirus E2 glycoprotein

C;Keywords: glycoprotein; peplomer protein; spike protein

F;1-520/Product: E2 glycoprotein subunit S1 #status predicted <GS1>

F;5;84,121,127,146,161,195,220,247,254,259,262,289,408,430,496,513/Binding site: carboxy

Query Match 31.1%; Score 51; DB 2; Length 520;

Best Local Similarity 46.7%; Pred. No. 22;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 YDINYTSEPCQKIN 24

|-:|:|:|:|:|:|

Db 464 YGLNYYKVNPCEDVN 478

RESULT 15

S14598

E2 glycoprotein - avian infectious bronchitis virus (strain UK/167/84)

N;Alternate names: spike glycoprotein chain S1

C;Species: avian infectious bronchitis virus, IBV

A;Variety: strain UK/167/84

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999

C;Accession: S14598

R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G. submitted to the EMBL Data Library, March 1991

A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some

A;Reference number: S14598

A;Accession: S14598

A;Status: preliminary

A;Molecule type: genomic RNA

A;Residues: 1-520 <CAV>

A;Cross-references: EMBL:X58068; NID:g59031; PIDN:CAA41099.1; PID:g59032

C;Superfamily: coronavirus E2 glycoprotein

C;Keywords: glycoprotein; peplomer protein; spike protein

F;1-520/Product: E2 glycoprotein subunit S1 #status predicted <GS1>

F;5;84,121,127,146,161,195,220,247,254,259,262,289,408,430,496,513/Binding site: carboxy

Query Match 31.1%; Score 51; DB 2; Length 520;

Best Local Similarity 46.7%; Pred. No. 22;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 YDINYTSEPCQKIN 24

|-:|:|:|:|:|:|

Db 464 YGLNYYKVNPCEDVN 478

A;Accession: S14598
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-520 <CAV>
A;Cross-references: EMBL:X58065; NID:g59025; PIDN:CAA41096.1; PID:g59026
C;Superfamily: coronavirus E2 glycoprotein

Query Match 31.1%; Score 51; DB 2; Length 520;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 YDINYYTSEPQOKIN 24
| : ||| | : : |
Db 464 YGLNYYKVNPCEDVN 478

Search completed: July 29, 2004, 13:30:11
Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:24:41 ; Search time 14 Seconds
(without alignments)
115.298 Million cell updates/sec

Title: US-09-852-238A-5
Perfect score: 164
Sequence: 1 MDYQVSSPIYDINITYTSPQCXKINVKQIAAR 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database : SwissProt 42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	164	100.0	352	1	P51681 homo sapien
2	159	97.0	352	1	P56440 pan troglod
3	154	93.9	352	1	Q97v42 cercopithec
4	154	93.9	352	1	Q62743 cercopithec
5	154	93.9	352	1	Q95nc5 hylobates s
6	154	93.9	352	1	P79436 macaca mula
7	154	93.9	352	1	P56441 papio hamad
8	154	93.9	352	1	Q97881 pongo pygma
9	153	93.3	352	1	Q97880 pygathrix b
10	153	93.3	352	1	Q97882 pygathrix n
11	153	93.3	352	1	Q97879 trachypithe
12	153	93.3	352	1	Q97878 trachypithe
13	149	90.9	352	1	P56439 gorilla gor
14	147	89.6	352	1	Q95nc0 hylobates m
15	145	88.4	352	1	P56493 cercopithec
16	144	87.8	352	1	Q97883 hylobates l
17	105	64.0	354	1	P51682 mus musculu
18	105	64.0	354	1	Q08556 rattus norv
19	55.5	33.8	373	1	P51683 mus musculu
20	55.5	33.8	373	1	Q05193 rattus norv
21	54.5	33.2	137	1	Q93251 arabidopsis
22	54.5	33.2	139	1	Q92sk3 arabidopsis
23	54	32.9	211	1	Q92ec9 lactococcus
24	54	32.9	211	1	P50926 lactococcus
25	53.5	32.6	139	1	Q9fvi2 petunia hyb
26	53.5	32.6	146	1	Q92sk2 arabidopsis
27	53	32.3	143	1	Q9sag3 vitis vinif
28	53	32.3	516	1	Q14360 schizosacch
29	52	31.7	1162	1	P2650 avian infec
30	52	31.7	1790	1	P11046 drosophila
31	51	31.1	139	1	Q39250 arabidopsis
32	51	31.1	520	1	P30206 avian infec
33	51	31.1	520	1	P30207 avian infec

RESULT 1

CKR5_HUMAN

ID CKR5_HUMAN STANDARD: PRT; 352 AA.

AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;

AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;

AC O14708; O15538; Q9UPA4;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)

DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).

DE CCR5 OR CMKBR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96241590; PubMed=8639485;

RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;

RT "Molecular cloning and functional expression of a new human

CC-chemokine receptor gene."

RL Biochemistry 35:3362-3367(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96291862; PubMed=8663314;

RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;

RT "Molecular cloning and functional characterization of a novel human

CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."

RL J. Biol. Chem. 271:17161-17166(1996).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=96295970; PubMed=8699119;

RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;

RT "Cloning and functional expression of CC CKR5, a human monocyte CC

chemokine receptor selective for Mip-1(alpha), Mip-1(beta), and

RANTES."

RL J. Leukoc. Biol. 60:147-152(1996).

RN [4]

RP SEQUENCE FROM N.A.

RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gao J., la Bastide M., Kaplan N., Greco T., Touchman J.,

Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,

Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,

Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,

Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;

Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA MEDLINE=98001387; PubMed=9343222;

RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;

RT "Polymorphisms in the CCR5 genes of African green monkeys and mice

implicate specific amino acids in infections by simian and human

immunodeficiency viruses."

RL J. Virol. 71:8642-8656(1997).

P30208 avian infec
P17662 avian infec
P12722 avian infec
P11223 avian infec
P05135 avian infec
Q8p215 streptococ
Q9f5u1 streptococ
Q8a6m0 bacteroides
O18793 macaca mula
P41597 homo sapien
P30174 brassica na
Q01031 herpesvirus

ALIGNMENTS

RN [6] SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RP MEDLINE=98022612; PubMed=9359654;
 RX Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 with 5'-end heterogeneity, dual promoter usage, and evidence for
 polymorphisms within the regulatory regions and noncoding exons.";
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260017; PubMed=8649511;
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhardt M.,
 RA di Marzio P., Mamon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 HIV-1.";
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 CC-CR5-5.";
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION.
 RX MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 entry.";
 RL Cell 96:667-676(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation. Acts as co-receptor with CD4 for primary non-
 CC syncytium-inducing strains (NGI) (macrophage-tropic) of HIV-1
 CC virus. It promotes Env-mediated fusion of the virus.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
 CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
 CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
 CC glycosylation.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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CC EMBL; X91492; CAA62796.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AAB17071.1; -
 DR EMBL; U95626; AAB57793.1; -
 DR EMBL; U83326; AAC51797.1; -
 DR EMBL; AF011500; AAB65700.1; -
 DR EMBL; AF011501; AAB65701.1; -
 DR EMBL; AF011502; AAB65702.1; -
 DR EMBL; AF011503; AAB65703.1; -
 DR EMBL; AF011505; AAB65705.1; -
 DR EMBL; AF011506; AAB65706.1; -
 DR EMBL; AF011507; AAB65707.1; -
 DR EMBL; AF011508; AAB65708.1; -
 DR EMBL; AF011509; AAB65709.1; -
 DR EMBL; AF011510; AAB65710.1; -
 DR EMBL; AF011511; AAB65711.1; -
 DR EMBL; AF011512; AAB65712.1; -
 DR EMBL; AF011513; AAB65713.1; -
 DR EMBL; AF011514; AAB65714.1; -
 DR EMBL; AF011515; AAB65715.1; -
 DR EMBL; AF011516; AAB65716.1; -
 DR EMBL; AF011517; AAB65717.1; -
 DR EMBL; AF011518; AAB65718.1; -
 DR EMBL; AF011519; AAB65719.1; -
 DR EMBL; AF011520; AAB65720.1; -
 DR EMBL; AF011521; AAB65721.1; -
 DR EMBL; AF011522; AAB65722.1; -
 DR EMBL; AF011523; AAB65723.1; -
 DR EMBL; AF011524; AAB65724.1; -
 DR EMBL; AF011525; AAB65725.1; -
 DR EMBL; AF011526; AAB65726.1; -
 DR EMBL; AF011527; AAB65727.1; -
 DR EMBL; AF011528; AAB65728.1; -
 DR EMBL; AF011529; AAB65729.1; -
 DR EMBL; AF011530; AAB65730.1; -
 DR EMBL; AF011531; AAB65731.1; -
 DR EMBL; AF011532; AAB65732.1; -
 DR EMBL; AF011533; AAB65733.1; -
 DR EMBL; AF011534; AAB65734.1; -
 DR EMBL; AF011535; AAB65735.1; -
 DR EMBL; AF011536; AAB65736.1; -
 DR EMBL; AF011537; AAB65737.1; -
 DR EMBL; AF011237; AAB94735.1; -
 DR EMBL; AF052539; AAD18131.1; -
 DR EMBL; AY221093; AAO65971.1; -
 DR Genew; HGNC:1606; CCR5.
 DR MIM; 601373; -
 DR GO; GO:0005768; C: endosome; TAS.
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0016493; F: C-C chemokine receptor activity; NAS.
 DR GO; GO:0015026; F: coreceptor activity; TAS.
 DR GO; GO:0007267; F: cell-cell signaling; TAS.
 DR GO; GO:0006968; F: cellular defense response; TAS.
 DR GO; GO:0006935; F: chemotaxis; TAS.
 DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signaling; TAS.
 DR GO; GO:0006954; P: inflammatory response; TAS.
 DR GO; GO:0007125; P: invasive growth; TAS.
 DR GO; GO:0007203; P: phosphatidylinositol-4,5-bisphosphate hydrolysis; TAS.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 164; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.8e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 2

ID CKR5 PANTR STANDARD; PRT; 352 AA.

AC P56440; 002778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CC5 OR CMKERS
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97426118; PubMed=9282822;
 RA Zacharova V., Zachar V., Goustin A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Buter C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).

CC EMBL; AF005663; AAB62557.1; -
 CC EMBL; U94329; AAB58446.1; -
 CC EMBL; AF011542; AAB65742.1; -
 CC EMBL; U97666; AAC51670.1; -
 CC EMBL; AF011540; AAB65740.1; -
 CC EMBL; U89797; AAC03717.1; -
 CC EMBL; AF177894; AAK43377.1; -
 CC InterPro: IPR00276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 97.0%; Score 159; DB 1; Length 352;
 Best Local Similarity 96.8%; Pred. No. 3e-15;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
 DB 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAAR 31

RESULT 3

CKR5_CERP STANDARD; PRT; 352 AA.

AC Q9TV42;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CC5 OR CMKERS.
 OS Cercopithecus pygerythrus (Vervet monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STEIN=100;
 RX MEDLINE=99335215; PubMed=10408730;
 RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
 RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
 RT "Mutations in CCR5-coding sequences are not associated with SIV
 RT carrier status in African nonhuman primates.";

RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 DR EMBL; AF053222; AD44015.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5)
GN CCR5 OR CMKBR5.
OS Hylobates syndactylus (Siamaung) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL: AF177884; ABA43367.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 7 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;
Query Match 93.9%; Score 154; DB 1; Length 352;
Best Local Similarity 93.5%; Pred. No. 1.5e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPTDYIDYITSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPTDYIDYITSEPCQKINVKQIAAR 31
RESULT 6
ID CCR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
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```
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5)
GN CCR5 OR CMKBR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=M.mulatta;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Sanson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: U77672; AAC51109.1; -.
CC EMBL: U73739; AAC51158.1; -.
CC EMBL: U96762; AAC34132.1; -.
CC EMBL: AF005660; AAB62554.1; -.
CC EMBL: AF005661; AAB62555.1; -.
CC EMBL: AF005662; AAB62556.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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DR PROSITE; PS0262; G-PROTEIN RECEPTOR; Transmembrane; Glycoprotein; Sulfation.
 KW G-protein coupled receptor; EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 241 241
 FT CONFLICT 292 292
 SQ SEQUENCE 352 AA; 40507 MW; 5896C85909FACB2 CRC64;

Query Match 93.9%; Score 154; DB 1; Length 352;
 Best Local Similarity 93.5%; Pred. No. 1.5e-14;
 Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKQKINVKQIAAR 31
 Db 1 MDYQVSSPTDYDIDYTSPPCKQKINVKQIAAR 31

RESULT 7
 ID CKR5 PAPH A STANDARD; PRT; 352 AA.
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OC NCBI TaxID=9557, 9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
 RA Shaaron M., Samson M., Lu Z.H., Clements J.B., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:400S-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates."
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.anubis;
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
 CC !- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.
 CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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CC EMBL; AF005658; AAB62552.1; -
 CC EMBL; AF105287; AAD20556.1; -
 CC EMBL; AF105288; AAD20557.1; -
 CC EMBL; AF105289; AAD20558.1; -
 CC EMBL; AF105290; AAD20559.1; -
 CC EMBL; AF023452; AAC63830.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 241 241
 FT CONFLICT 292 292
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1F8B2 CRC64;

Query Match 93.9%; Score 154; DB 1; Length 352;
 Best Local Similarity 93.5%; Pred. No. 1.5e-14;
 Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKQKINVKQIAAR 31
 Db 1 MDYQVSSPTDYDIDYTSPPCKQKINVKQIAAR 31

RESULT 8
 ID CKR5 PONPY STANDARD; PRT; 352 AA.
 AC O97881;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Pongo pygmaeus (Orangutan).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

```

OC NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
CC PROSITE; PS0262; G PROTEIN RECP FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT DOMAIN 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 93.9%; Score 154; DB 1; Length 352;
Best Local Similarity 93.5%; Pred. No. 1.5e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
| | | | | | | | | | | | | | | | | | | |
Db 1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAAR 31
| | | | | | | | | | | | | | | | | | | |

RESULT 9
CCRS_PYGBI
ID CCR5_PYGBI STANDARD; PRT; 352 AA.
AC O97850;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

```

```

OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
CC PROSITE; PS0262; G PROTEIN RECP FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 93.3%; Score 153; DB 1; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.1e-14;
Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
| | | | | | | | | | | | | | | | | | | |
Db 1 MDYQVSSPTIDIDYYTSEPCQKINVKQIAAR 31
| | | | | | | | | | | | | | | | | | | |

RESULT 10
CCRS_PYGNE
ID CCR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075448; AAD19860.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRRHODOPSIN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89 2 (POTENTIAL).
CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124 3 (POTENTIAL).
CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166 4 (POTENTIAL).
CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218 5 (POTENTIAL).
CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260 6 (POTENTIAL).
CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301 7 (POTENTIAL).
CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 101 178 BY SIMILARITY.
CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3861 CRC64;
SQ
Query Match 93.3%; Score 153; DB 1; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.1e-14;
Matches 28; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSFPCQKINVKQIAAR 31
DB 1 MDYQVSSPTDIDYTSFPCQKINVKQIAAR 31

RESULT 11
CKR5_TRAFR
ID CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075442; AAD19854.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRRHODOPSIN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89 2 (POTENTIAL).
CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124 3 (POTENTIAL).
CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166 4 (POTENTIAL).
CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218 5 (POTENTIAL).
CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260 6 (POTENTIAL).
CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301 7 (POTENTIAL).
CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 101 178 BY SIMILARITY.
CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;
SQ
Query Match 93.3%; Score 153; DB 1; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.1e-14;
Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSFPCQKINVKQIAAR 31
DB 1 MDYQVSSPTDIDYTSFPCQKINVKQIAAR 31

RESULT 12
CKR5_TRAFR
ID CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.

```


Os Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 ON NCBI_TaxID=61618;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL; AF075443; AAD19855.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 4 (POTENTIAL).
 FT TRANSMEM 142 166 5 (POTENTIAL).
 FT DOMAIN 167 198 6 (POTENTIAL).
 FT TRANSMEM 199 218 7 (POTENTIAL).
 FT DOMAIN 219 235 8 (POTENTIAL).
 FT TRANSMEM 236 260 9 (POTENTIAL).
 FT DOMAIN 261 277 10 (POTENTIAL).
 FT TRANSMEM 278 301 11 (POTENTIAL).
 FT DOMAIN 302 352 12 (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;
 Query Match 93.3%; Score 153; DB 1; Length 352;
 Best Local Similarity 90.3%; Pred. No. 2.1e-14; Indels 0; Gaps 0;
 Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPTIDYNTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPTIDYNTSEPCQKINVKQIAAR 31
 RESULT 13
 ID CCR5_GORGO STANDARD; PRT; 352 AA.
 AC P56439;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CCR5 OR CMKBR5.
 OS Gorilla gorilla gorilla (lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
 ON NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 CC simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AF005659; AAB62553.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 4 (POTENTIAL).
 FT TRANSMEM 142 166 5 (POTENTIAL).
 FT DOMAIN 167 198 6 (POTENTIAL).
 FT TRANSMEM 199 218 7 (POTENTIAL).
 FT DOMAIN 219 235 8 (POTENTIAL).
 FT TRANSMEM 236 260 9 (POTENTIAL).
 FT DOMAIN 261 277 10 (POTENTIAL).
 FT TRANSMEM 278 301 11 (POTENTIAL).
 FT DOMAIN 302 352 12 (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9F5EAC84 CRC64;
 Query Match 90.9%; Score 149; DB 1; Length 352;
 Best Local Similarity 90.3%; Pred. No. 8e-14; Indels 0; Gaps 0;
 Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDYQVSSPTIDYNTSEPCQKINVKQIAAR 31
 Db 1 MDYQVSSPTIDYNTSEPCQKINVKQIAAR 31
 RESULT 14
 ID CCR5_HYMLM STANDARD; PRT; 352 AA.
 AC Q95NC0;
 DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DN C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF177899; AAK43382.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 6 (POTENTIAL).
FT TRANSMEM 236 260 7 (POTENTIAL).
FT DOMAIN 261 277 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 278 301 BY SIMILARITY.
FT DISULFID 302 352 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;
Query Match 89.6%; Score 147; DB 1; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.5e-13;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAAR 31
RESULT 15
CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U83324; AAC51795.1; -
CC EMBL; U83325; AAC51796.1; -
CC EMBL; AB015944; BAA31328.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 6 (POTENTIAL).
FT TRANSMEM 236 260 7 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 BY SIMILARITY.
FT DISULFID 302 352 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT VARIANT 352 352 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;
Query Match 88.4%; Score 145; DB 1; Length 352;

Best Local Similarity 90.3%; Pred. No. 2.9e-13;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSFTYDIDNVTSEPCQKINVKQIAAR 31

Search completed: July 29, 2004, 13:28:57
Job time : 15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:25:16 ; Search time 35 Seconds
(without alignments)
279.459 Million cell updates/sec

Title: US-09-852-238A-5

Perfect score: 164

Sequence: 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	100.0	215	4	075303
2	159	97.0	352	6	Q95NC3
3	159	97.0	352	6	O18771
4	159	97.0	352	6	O18772
5	159	97.0	352	6	Q9TQX0
6	154	93.9	344	6	Q9TQR8
7	154	93.9	344	6	O77833
8	154	93.9	352	6	Q9TSK1
9	154	93.9	352	6	Q95NC5
10	154	93.9	352	6	Q9TV48
11	154	93.9	352	6	Q9TV49
12	154	93.9	352	6	O9XT76
13	154	93.9	352	6	O18770
14	154	93.9	352	6	Q9TV44
15	154	93.9	352	6	Q97975
16	154	93.9	352	6	Q9XT12

17	154	93.9	352	6	Q9TV42
18	154	93.9	352	6	Q9XT13
19	154	93.9	352	6	Q95ND2
20	154	93.9	352	6	O77776
21	154	93.9	352	6	Q9TV46
22	154	93.9	352	6	Q9TSQ7
23	154	93.9	352	6	Q9MZA2
24	154	93.9	352	6	Q9TV50
25	154	93.9	352	6	Q9TV45
26	154	93.9	352	6	Q95NE1
27	154	93.9	352	6	Q95ND0
28	154	93.9	352	6	Q95NE8
29	153	93.3	352	6	Q9XT14
30	153	93.3	352	6	Q95NC6
31	153	93.3	352	6	Q95NC8
32	153	93.3	352	6	Q95NC7
33	153	93.3	352	6	Q97962
34	150	91.5	352	6	Q95NC1
35	149	90.9	352	6	Q9XS35
36	149	90.9	352	6	Q9TV93
37	149	90.9	352	6	Q95ND1
38	149	90.9	352	6	Q9XS99
39	148	90.2	352	6	Q9TV43
40	147	89.6	352	6	Q95NC0
41	147	89.6	352	6	Q9MZA3
42	145	88.4	352	6	Q9TV47
43	145	88.4	352	6	Q9BGN5
44	145	88.4	352	6	Q9BGN6
45	129	78.7	339	4	Q9UN26

ALIGNMENTS

RESULT 1

075303 PRELIMINARY; PRT; 215 AA.

AC 075303; (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE CC-chemokine receptor.
GN CCR-5.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Tse L., Ehrenberg P.K., Chang G., Michael N.I.;
RT "Genomic Organization and Functional Characterization of the Complete Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-Receptor for HIV-1";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003962; AAC23944.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000186; P:G-protein coupled receptor protein signalin...; IEA.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.

SQ SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;

Query Match 100.0%; Score 164; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

|||||

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Db      1 MDYQVSSPIYDINYVTSEPCQKINVKQIAAR 31
RESULT 2
Q95NC3  PRELIMINARY;      PRT;      352 AA.
AC .Q95NC3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Miopithecus.
OX NCBI_TaxID=36231;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
  phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177886; AAK43369.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40546 MW; 6464152F3B566AB5 CRC64;

Query Match      97.0%; Score 159; DB 6; Length 352;
Best Local Similarity 96.8%; Pred. No. 4.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDYQVSSPIYDINYVTSEPCQKINVKQIAAR 31
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Db      1 MDYQVSSPIYDINYVTSEPCQKINVKQIAAR 31
      |||||

RESULT 3
Q18771  PRELIMINARY;      PRT;      352 AA.
AC Q18771;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011541; AAB65741.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match      97.0%; Score 159; DB 6; Length 352;
Best Local Similarity 96.8%; Pred. No. 4.4e-15;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDYQVSSPIYDINYVTSEPCQKINVKQIAAR 31
      |||||
Db      1 MDYQVSSPIYDINYVTSEPCQKINVKQIAAR 31
      |||||

RESULT 5
Q9TQX0  PRELIMINARY;      PRT;      352 AA.
AC Q9TQX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=AGM-8CCR5, AGM-3CCR5, and AGM-5CCR5;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483 (1999).
DR EMBL; AF105286; AAD20555.1; -.
DR EMBL; AF105284; AAD20553.1; -.
DR EMBL; AF105285; AAD20554.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40588 MW; 0A4E4119FAC8EC75 CRC64;
Query Match 97.0%; Score 159; DB 6; Length 352;
Best Local Similarity 96.8%; Pred. No. 4.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
RESULT 6
Q9TOR8 PRELIMINARY; PRT; 344 AA.
AC Q9TOR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine receptor CCR5.
GN CCR5.
OS Cercopithecus torquatus torquatus, and
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercocebus.
OX NCBI_TaxID=81944, 9531;
RN [1]_TaxID=81944, 9531;
RP SEQUENCE FROM N.A.
RC SPECIES=C.torquatus torquatus; STRAIN=1049, and 997;
RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
RA Aguilar R., Ho D.D., Marx P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
with a R2b-tropic simian immunodeficiency virus.";
RL J. Exp. Med. 0:0-0 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.torquatus atys;
RA Palacios E., Digilio L., McClure H.M., Chen Z., Marx P.A.,
RA Goldsmith M.A., Grant R.M.;
RT "Parallel evolution of CCR5-null phenotypes in humans and in a natural
host of simian immunodeficiency virus.";
RL Curr. Biol. 0:0-0 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=C.torquatus torquatus; STRAIN=RCM411;
RA Beer B.E., Kulken C.B., Tooze Z., Foley B.T., Goeken R.M., Brown C.R.,
RA St Claire M., Hirsch V.M.;
RT "Characterization of novel simian immunodeficiency viruses from
red-capped mangabey from Nigeria (SIVrcmNgM411 and NgD409).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF094753; AAC62474.1; -.
DR EMBL; AF079473; AAC31194.1; -.
DR EMBL; AF084003; AAC62471.1; -.

DR EMBL; AF349683; AAK69685.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 344 AA; 39592 MW; E15F5F601191A4D1 CRC64;
Query Match 93.9%; Score 154; DB 6; Length 344;
Best Local Similarity 93.5%; Pred. No. 2.3e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
RESULT 7
O77833 PRELIMINARY; PRT; 344 AA.
AC O77833;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine receptor CCR5.
GN CCR5.
OS Cercocebus torquatus torquatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercocebus.
OX NCBI_TaxID=81944;
RN [1]_TaxID=81944;
RP SEQUENCE FROM N.A.
RC STRAIN=1208, and 009;
RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
RA Aguilar R., Ho D.D., Marx P.A.;
RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
with a R2b-tropic simian immunodeficiency virus.";
RL J. Exp. Med. 0:0-0 (1998).
DR EMBL; AF094752; AAC62473.1; -.
DR EMBL; AF084002; AAC62470.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 344 AA; 39578 MW; 0CEC05E47C2F6DE6 CRC64;
Query Match 93.9%; Score 154; DB 6; Length 344;
Best Local Similarity 93.5%; Pred. No. 2.3e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
RESULT 8
Q9TSK1 PRELIMINARY; PRT; 352 AA.
AC Q9TSK1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G-protein coupled chemokine receptor.

```

OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Holtkamp N., Baier M., Werner A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF019379; AAD01639.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40588 MW; 0F1869D9A6668DBB CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
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DB 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAAR 31

RESULT 9
Q95NC5
ID Q95NC5 PRELIMINARY; PRT; 352 AA.
AC Q95NC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
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DB 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAAR 31

RESULT 10
Q9TV48

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ID Q9TV48 PRELIMINARY; PRT; 352 AA.
AC Q9TV48;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Cercopithecus ascanius (black-cheeked white-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36223;
RN [1]
RP SEQUENCE FROM N.A.
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RL Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
   carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RL Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035216; AAD44009.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40650 MW; 7906256AA3945266 CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
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DB 1 MDYQVSSPTYDIDYITSEPCQKINVKQIAAR 31

RESULT 11
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ID Q9TV49 PRELIMINARY; PRT; 352 AA.
AC Q9TV49;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor type 5 (C-C chemokine receptor 5).
GN CCR5.
OS Cercopithecus galenitus (Agile mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9532;
RN [1]
RP SEQUENCE FROM N.A.
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RL Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
   carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=04;
RA MEDLINE=99335215; PubMed=10408730;
RX Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=04;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035220; AAD44013.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40747 MW; 3A56E90D3528D94C CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPTDYDITYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPTDYDITYTSEPCQKINVKQIAAR 31

RESULT 15
O97975 PRELIMINARY; PRT; 352 AA.
AC O97975;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor type 5.
GN CCR5.
OS Macaca arctoides (Stump-tailed macaque), and
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9540, 9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075450; AAD19862.1; -
DR EMBL; AF075449; AAD19861.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40521 MW; 5F276C85909FACB2 CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MDYQVSSPTDYDITYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPTDYDITYTSEPCQKINVKQIAAR 31

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Job time : 36 secs
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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 164
Sequence: 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	164	100.0	87	3	US-09-087-232A-18
2	164	100.0	100	3	US-09-087-232A-15
3	164	100.0	184	4	US-08-833-752-4
4	164	100.0	215	3	US-09-087-232A-17
5	164	100.0	215	4	US-08-833-752-6
6	164	100.0	352	3	US-09-087-232A-13
7	164	100.0	352	3	US-08-861-105-14
8	164	100.0	352	3	US-08-575-967A-2
9	164	100.0	352	4	US-08-833-752-5
10	164	100.0	352	4	US-09-502-783A-2
11	164	100.0	352	4	US-09-796-202-1
12	159	97.0	352	3	US-09-045-583-52
13	159	97.0	352	4	US-09-534-185-52
14	158	96.3	352	3	US-08-466-343D-2
15	144	87.8	352	4	US-09-517-605-5
16	123	75.0	22	3	US-08-861-105-4
17	113	68.9	20	2	US-08-889-291-32
18	113	68.9	20	3	US-09-098-244-32
19	113	68.9	20	4	US-09-375-314-32
20	113	68.9	20	4	US-09-767-395-32
21	105	64.0	28	3	US-08-861-105-6
22	105	64.0	354	4	US-08-724-984A-2
23	81.5	49.7	26	4	US-09-131-827A-14
24	52	31.7	158	4	US-09-621-976-7413
25	51	31.1	705	2	US-08-663-566A-19
26	51	31.1	705	2	US-08-023-610-19
27	51	31.1	705	2	US-08-288-065A-19

28	51	31.1	705	2	US-08-362-240A-19	Sequence 19, Appl
29	51	31.1	705	5	PCT-US95-10245-19	Sequence 19, Appl
30	51	31.1	1130	4	US-09-242-435-4	Sequence 4, Appl
31	49	29.9	83	4	US-09-131-827A-13	Sequence 13, Appl
32	49	29.9	170	3	US-09-117-257-50	Sequence 50, Appl
33	49	29.9	170	4	US-09-489-352-50	Sequence 50, Appl
34	49	29.9	329	4	US-09-502-783A-9	Sequence 9, Appl
35	49	29.9	344	3	US-08-466-343D-9	Sequence 9, Appl
36	49	29.9	347	1	US-08-461-244-3	Sequence 3, Appl
37	49	29.9	360	1	US-08-450-393A-4	Sequence 4, Appl
38	49	29.9	360	3	US-08-446-669-4	Sequence 4, Appl
39	49	29.9	360	3	US-09-045-583-50	Sequence 50, Appl
40	49	29.9	360	3	US-09-045-583-51	Sequence 51, Appl
41	49	29.9	360	4	US-09-534-185-50	Sequence 50, Appl
42	49	29.9	360	4	US-09-534-185-51	Sequence 51, Appl
43	49	29.9	360	4	US-08-833-752-7	Sequence 7, Appl
44	49	29.9	360	4	US-09-131-827A-2	Sequence 2, Appl
45	49	29.9	360	4	US-09-131-827A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-087-232A-18
; Sequence 18, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 May 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 May 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-18

Query Match 100.0%; Score 164; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1e-17; 0;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

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RESULT 2
US-09-087-232A-15
; Sequence 15, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-15

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 3
US-08-833-752-4
; Sequence 4, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 4
US-09-087-232A-17
; Sequence 17, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-17

Query Match 100.0%; Score 164; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 4
US-09-087-232A-17
; Sequence 17, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-17
```

```
Query Match 100.0%; Score 164; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 5
US-08-833-752-6
; Sequence 6: Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: 6:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-6

Query Match 100.0%; Score 164; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 6
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA

Query Match 100.0%; Score 164; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYTSEPCQKINVKQIAAR 31

RESULT 7
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELMMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 164; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31

RESULT 8
US-08-575-967A-2
Sequence 2, Application US/08575967A
Patent No. 6511825
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 164; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31
RESULT 9
US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-833-752-5

Query Match 100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31
DB 1 MDYQVSSPIYDINVTSEPCQKINVKQIAAR 31

RESULT 10
US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. 6511825
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR
TITLE OF INVENTION: HDGMR10
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 164; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

RESULT 12
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207

```

```

; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match      97.0%; Score 159; DB 3; Length 352;
Best Local Similarity 96.8%; Pred. No. 3.1e-16;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDIDYTTSEPCQKINVKQIAAR 31

RESULT 13
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match      97.0%; Score 159; DB 4; Length 352;
Best Local Similarity 96.8%; Pred. No. 3.1e-16;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAAR 31

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Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAAR 31

RESULT 14

US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGHR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STERPE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 96.3%; Score 158; DB 3; Length 352;
Best Local Similarity 96.8%; Pred. No. 4.5e-16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAAR 31

RESULT 15

US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-517-605-5

Query Match 87.8%; Score 144; DB 4; Length 352;
Best Local Similarity 90.3%; Pred. No. 6e-14;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAAR 31
Db 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAAR 31

Search completed: July 29, 2004, 13:30:40
Job time : 19 secs